

SEQUENCE LISTING

<110> Sprecher, Cindy A.
 Presnell, Scott R.
 Gao, Zeren
 Whitmore, Theodore E.
 Kuijper, Joseph L.
 Maurer, Mark F.

<120> CYTOKINE RECEPTOR ZCYTOR17

<130> 00-42

<150> US 60/214,282

<151> 2000-06-26

<150> US 60/214,955

<151> 2000-06-29

<150> US 60/267,963

<151> 2001-08-02

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aatgtccgca aaacattctc tctccccagc ctctcatgtgt taacctgggg atg atg      176
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Arg Lys Asn Leu Thr Cys Thr Trp Ser Pro Ala Gly Lys Glu Thr Ser Tyr
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Thr Gln Tyr Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys His Asp
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Trp Met Ile Glu Trp Phe Pro Asp Val Asp Ser Glu Pro Thr Thr Leu			
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Ser Trp Glu Ser Val Ser Gln Ala Thr Asn Trp Thr Ile Gln Gln Asp			
375 380 385			
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Lys Leu Lys Pro Phe Trp Cys Tyr Asn Ile Ser Val Tyr Pro Met Leu			
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His Asp Lys Val Gly Glu Pro Tyr Ser Ile Gln Ala Tyr Ala Lys Glu			
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Gly Val Pro Ser Glu Gly Pro Glu Thr Lys Val Glu Asn Ile Gly Val			
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Lys Thr Val Thr Ile Thr Trp Lys Glu Ile Pro Lys Ser Glu Arg Lys			
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Gly Ile Ile Cys Asn Tyr Thr Ile Phe Tyr Gln Ala Glu Gly Gly Lys			
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Gly Phe Ser Lys Thr Val Asn Ser Ser Ile Leu Gln Tyr Gly Leu Glu			
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Ser Leu Lys Arg Lys Thr Ser Tyr Ile Val Gln Val Met Ala Ser Thr			
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Ser Ala Gly Gly Thr Asn Gly Thr Ser Ile Asn Phe Lys Thr Leu Ser			
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Phe Ser Val Phe Glu Ile Ile Leu Ile Thr Ser Leu Ile Gly Gly Gly			
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Ser Ser Ile Ala Thr Trp His Gly Asp Asp Phe Lys Asp Lys Leu Asn			
565 570 575			

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Pro Cys Ser Thr Pro Ser Asp Lys Leu Val Ile Asp Lys Leu Val Val	
595 600 605 610	
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Gly Gln Glu Asn Asn Leu Gly Gly Glu Lys Asn Gly Tyr Val Thr Cys	
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Val Ser Pro Glu Ile Pro Pro Arg Lys Ser Gln Tyr Leu Arg Ser Arg	
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Gly Gln Ser Leu Val Pro Asp His Leu Cys Glu Glu Gly Ala Pro Asn	
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aaa ctt cca gag cac acc aag gga gaa gtc taaatgcgac catagcátga	2386
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Ser Tyr Thr Gln Tyr Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys	
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Cys Ser Phe Phe Leu Pro Arg Ile Thr Ile Pro Asp Asn Tyr Thr Ile	
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Lys	Asn	Arg	Lys	Asp	Lys	Asn	Gln	Thr	Tyr	Asn	Leu	Thr	Gly	Leu	Gln
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Ala	Pro	Val	Leu	Glu	Lys	Thr	Leu	Gly	Tyr	Asn	Ile	Trp	Tyr	Tyr	Pro
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Ile	Gln	Glu	Lys	Ser	Phe	Gln	Cys	Ile	Glu	Val	Met	Gln	Ala	Cys	Val
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Ala	Glu	Asp	Gln	Leu	Val	Val	Lys	Trp	Gln	Ser	Ser	Ala	Leu	Asp	Val
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 625 630 635 640
 Thr Cys Pro Phe Arg Pro Asp Cys Pro Leu Gly Lys Ser Phe Glu Glu
 645 650 655
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 Ser Arg Met Pro Glu Gly Thr Arg Pro Glu Ala Lys Glu Gln Leu Leu
 675 680 685
 Phe Ser Gly Gln Ser Leu Val Pro Asp His Leu Cys Glu Glu Gly Ala
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 aaracngarc cncncaarat htymngngtn aarccngtny tnggnathaa rmgnatgath 420
 carathgart ggathaarcc ngarytngcn ccngtnwsnw sngayytnaa rtayacnytn 480
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 gayaaraayc aracntayaa yytnacnggn ytnarcnt tyacngarta ygtnathgcn 600
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 gcngayggnm gnmngccngt nmngnytnytn tggaaraarg cnmgngggngc nccngtnytn 780
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24

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<223> Oligonucleotide primer ZC5020

<400> 15
cactggagtg gcaacttcca g 21

<210> 16
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<212> DNA
<213> Homo sapiens

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gcctttttaca gaatatgtca tagctctgcg atgtgcggtc aaggagtcaa agttctggag 120
tgactggagc caagaaaaaa tgggaatgac tgaggaagaa gctccatgtg gcctggaact 180
gtggggagtc ctgaaaccag ctgaggcgga tgggaagaagg ccagtgcggt tggtatggaa 240
gaaggcaaga ggagcccccag tcctagagaa aacacttgge tacaacatat ggtactatcc 300
agaaagcaac actaacctca cagaaacaat gaacactact aaccagcagc ttgaactgca 360
tctgggaggc gagagctttt ggtgtcttat gatttcttat aattctcttg ggaagtctcc 420
agtggccacc ctgaggattc cagctattca agaaaaatca tttcagtgca ttgagggtcat 480
gcaggcctgc gttgctgagg accagctagt ggtgaagtgg caaagctctg ctctagacgt 540
gaacacttgg atgattgaat ggtttccgga tgtggactca gagcccacca ccctttcctg 600
ggaatctgtg tctcaggcca cgaactggac gatccagcaa gataaattaa aacctttctg 660
gtgctataac atctctgtgt atccaatgtt gcatgacaaa gttggcgagc catattccat 720
ccaggcttat gccaaagaag gcgttccatc agaaggtcct gagaccaagg tggagaacat 780
tggcgtgaag acggtcacga tcacatggag agagattccc aagagtgaga gaaaggggat 840
catctgcaac tacaccatct tttaccaagc tgaaggtgga aaaggattct ccaagacagt 900
caattccagc atcttgcagt acggcctgga gtccctgaaa cgaaagacct cttacattgt 960
tcaggctatg gccagcacca gtgctggggg aaccaacggg accagcataa atttcaagac 1020
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aggaggggaa aagaatggga ctagaattct gtcttctctgc ccaacttcaa tataagtgtg 1440
gactaaaatg cgagaaagggt gtcctgtggg ctatgcaaat tagaaaggac atgcagagtt 1500
ttccaactag gaagactgaa tctgtggccc caagagaacc atctctgaag actgggtatg 1560

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tgggtcttttc cacacatgga ccacctacgg atgtaatctg taatgcatgt gcatgagaag 1620
tctgttatta agtagagtgt gaaaacatgg ttatggtaat aggaacagct tttaaaatgc 1680
ttttgcattt gggcctttca tacaaaaaag ccataatacc attttcatgt aatgctatac 1740
ttctatacta ttttcatgta atactatact tctatactat tttcatgtaa tactatactt 1800
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<210> 17
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<212> DNA
<213> Homo sapiens

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<222> (162)...(1133)

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aaaacattct ctctccccag ctttcatgtg ttaacctggg g atg atg tgg acc tgg 176
Met Met Trp Thr Trp
1 5

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gca ctg tgg atg ctc ccc tca ctc tgc aaa ttc agc ctg gca gct ctg 224
Ala Leu Trp Met Leu Pro Ser Leu Cys Lys Phe Ser Leu Ala Ala Leu
10 15 20

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cca gct aag cct gag aac att tcc tgt gtc tac tac tat agg aaa aat 272
Pro Ala Lys Pro Glu Asn Ile Ser Cys Val Tyr Tyr Tyr Arg Lys Asn
25 30 35

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tta acc tgc act tgg agt cca gga aag gaa acc agt tat acc cag tac 320
Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu Thr Ser Tyr Thr Gln Tyr
40 45 50

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aca gtt aag aga act tac gct ttt gga gaa aaa cat gat aat tgt aca 368
Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys His Asp Asn Cys Thr
55 60 65

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acc aat agt tct ada agt gaa aat cgt gct tgc tgc tct ttt ttc ctt 416
Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala Ser Cys Ser Phe Phe Leu
70 75 80 85

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cca aga ata acg atc cca gat aat tat acc att gag gtg gaa gct gaa 464
Pro Arg Ile Thr Ile Pro Asp Asn Tyr Thr Ile Glu Val Glu Ala Glu
90 95 100

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aat gga gat ggt gta att aaa tct cat atg aca tac tgg aga tta gag 512
Asn Gly Asp Gly Val Ile Lys Ser His Met Thr Tyr Trp Arg Leu Glu
105 110 115

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aac ata gcg aaa act gaa cca cct aag att ttc cgt gtg aaa cca gtt 560
Asn Ile Ala Lys Thr Glu Pro Pro Lys Ile Phe Arg Val Lys Pro Val
120 125 130

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ttg ggc atc aaa cga atg att caa att gaa tgg ata aag cct gag ttg 608
Leu Gly Ile Lys Arg Met Ile Gln Ile Glu Trp Ile Lys Pro Glu Leu
135 140 145

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gcg cct gtt tca tct gat tta aaa tac aca ctt cga ttc agg aca gtc 656
Ala Pro Val Ser Ser Asp Leu Lys Tyr Thr Leu Arg Phe Arg Thr Val
150 155 160 165

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aac agt acc agc tgg atg gaa gtc aac ttc gct aag aac cgt aag gat Asn Ser Thr Ser Trp Met Glu Val Asn Phe Ala Lys Asn Arg Lys Asp 170 175 180	704
aaa aac caa acg tac aac ctc acg ggg ctg cag cct ttt aca gaa tat Lys Asn Gln Thr Tyr Asn Leu Thr Gly Leu Gln Pro Phe Thr Glu Tyr 185 190 195	752
gtc ata gct ctg cga tgt gcg gtc aag gag tca aag ttc tgg agt gac Val Ile Ala Leu Arg Cys Ala Val Lys Glu Ser Lys Phe Trp Ser Asp 200 205 210	800
tgg agc caa gaa aaa atg gga atg act gag gaa gaa gct cca tgt ggc Trp Ser Gln Glu Lys Met Gly Met Thr Glu Glu Glu Ala Pro Cys Gly 215 220 225	848
ctg gaa ctg tgg aga gtc ctg aaa cca gct gag gcg gat gga aga agg Leu Glu Leu Trp Arg Val Leu Lys Pro Ala Glu Ala Asp Gly Arg Arg 230 235 240 245	896
cca gtg cgg ttg tta tgg aag aag gca aga gga gcc cca gtc cta gag Pro Val Arg Leu Leu Trp Lys Lys Ala Arg Gly Ala Pro Val Leu Glu 250 255 260	944
aaa aca ctt ggc tac aac ata tgg tac tat cca gaa agc aac act aac Lys Thr Leu Gly Tyr Asn Ile Trp Tyr Tyr Pro Glu Ser Asn Thr Asn 265 270 275	992
ctc aca gaa aca atg aac act act aac cag cag ctt gaa ctg cat ctg Leu Thr Glu Thr Met Asn Thr Thr Asn Gln Gln Leu Glu Leu His Leu 280 285 290	1040
gga ggc gag agc ttt tgg gtg tct atg att tct tat aat tct ctt ggg Gly Gly Glu Ser Phe Trp Val Ser Met Ile Ser Tyr Asn Ser Leu Gly 295 300 305	1088
aag tct cca gtg gcc acc ctg agg att cca gct att caa gaa aaa Lys Ser Pro Val Ala Thr Leu Arg Ile Pro Ala Ile Gln Glu Lys 310 315 320	1133
tagaaacttt acagatgcta gtcccagaca taaaagaaaa taatgttctg gatgtgcacg atggctcacg cctgtaatcc cagcactttg aggccaagac gggtggatcg ctgagttcag gagttcaaga caagtccagg caacatagtg aaaccttggt tctaca	1193 1253 1299

<210> 18
 <211> 324
 <212> PRT
 <213> Homo sapiens

<400> 18

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Ser Leu Ala Ala Leu Pro Ala Lys Pro Glu Asn Ile Ser Cys Val Tyr 20 25 30
Tyr Tyr Arg Lys Asn Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu Thr 35 40 45
Ser Tyr Thr Gln Tyr Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys 50 55 60
His Asp Asn Cys Thr Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala Ser 65 70 75 80
Cys Ser Phe Phe Leu Pro Arg Ile Thr Ile Pro Asp Asn Tyr Thr Ile 85 90 95

Glu Val Glu Ala Glu Asn Gly Asp Gly Val Ile Lys Ser His Met Thr
 100 105 110
 Tyr Trp Arg Leu Glu Asn Ile Ala Lys Thr Glu Pro Pro Lys Ile Phe
 115 120 125
 Arg Val Lys Pro Val Leu Gly Ile Lys Arg Met Ile Gln Ile Glu Trp
 130 135 140
 Ile Lys Pro Glu Leu Ala Pro Val Ser Ser Asp Leu Lys Tyr Thr Leu
 145 150 155 160
 Arg Phe Arg Thr Val Asn Ser Thr Ser Trp Met Glu Val Asn Phe Ala
 165 170 175
 Lys Asn Arg Lys Asp Lys Asn Gln Thr Tyr Asn Leu Thr Gly Leu Gln
 180 185 190
 Pro Phe Thr Glu Tyr Val Ile Ala Leu Arg Cys Ala Val Lys Glu Ser
 195 200 205
 Lys Phe Trp Ser Asp Trp Ser Gln Glu Lys Met Gly Met Thr Glu Glu
 210 215 220
 Glu Ala Pro Cys Gly Leu Glu Leu Trp Arg Val Leu Lys Pro Ala Glu
 225 230 235 240
 Ala Asp Gly Arg Arg Pro Val Arg Leu Leu Trp Lys Lys Ala Arg Gly
 245 250 255
 Ala Pro Val Leu Glu Lys Thr Leu Gly Tyr Asn Ile Trp Tyr Tyr Pro
 260 265 270
 Glu Ser Asn Thr Asn Leu Thr Glu Thr Met Asn Thr Thr Asn Gln Gln
 275 280 285
 Leu Glu Leu His Leu Gly Gly Glu Ser Phe Trp Val Ser Met Ile Ser
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<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC27897

<400> 19

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<211> 22

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<213> Artificial Sequence

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<223> Oligonucleotide primer ZC28521

<400> 20

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22

<210> 21

<211> 1476

<212> DNA

<213> Homo sapiens

<220>

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<222> (162)...(878)

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aaaacattct ctctccccag ccttcatgtg ttaacctggg g atg atg tgg acc tgg	176
Met Met Trp Thr Trp	
1 5	
gca ctg tgg atg ctc ccc tca ctc tgc aaa ttc agc ctg gca gct ctg	224
Ala Leu Trp Met Leu Pro Ser Leu Cys Lys Phe Ser Leu Ala Ala Leu	
10 15 20	
cca gct aag cct gag aac att tcc tgt gtc tac tac tat agg aaa aat	272
Pro Ala Lys Pro Glu Asn Ile Ser Cys Val Tyr Tyr Tyr Arg Lys Asn	
25 30 35	
tta acc tgc act tgg agt cca gga aag gaa acc agt tat acc cag tac	320
Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu Thr Ser Tyr Thr Gln Tyr	
40 45 50	
aca gtt aag aga act tac gct ttt gga gaa aaa cat gat aat tgt aca	368
Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys His Asp Asn Cys Thr	
55 60 65	
acc aat agt tct aca agt gaa aat cgt gct tgc tgc tct ttt ttc ctt	416
Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala Ser Cys Ser Phe Phe Leu	
70 75 80 85	
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Pro Arg Ile Thr Ile Pro Asp Asn Tyr Thr Ile Glu Val Glu Ala Glu	
90 95 100	
aat gga gat ggt gta att aaa tct cat atg aca tac tgg aga tta gag	512
Asn Gly Asp Gly Val Ile Lys Ser His Met Thr Tyr Trp Arg Leu Glu	
105 110 115	
aac ata gcg aaa act gaa cca cct aag att ttc cgt gtg aaa cca gtt	560
Asn Ile Ala Lys Thr Glu Pro Pro Lys Ile Phe Arg Val Lys Pro Val	
120 125 130	
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Leu Gly Ile Lys Arg Met Ile Gln Ile Glu Trp Ile Lys Pro Glu Leu	
135 140 145	
gcg cct gtt tca tct gat tta aaa tac aca ctt cga ttc agg aca gtc	656
Ala Pro Val Ser Ser Asp Leu Lys Tyr Thr Leu Arg Phe Arg Thr Val	
150 155 160 165	
aac agt acc agc tgg atg gaa gtc aac ttc gct aag aac cgt aag gat	704
Asn Ser Thr Ser Trp Met Glu Val Asn Phe Ala Lys Asn Arg Lys Asp	
170 175 180	
aaa aac caa acg tac aac ctc acg ggg ctg cag cct ttt aca gaa tat	752
Lys Asn Gln Thr Tyr Asn Leu Thr Gly Leu Gln Pro Phe Thr Glu Tyr	
185 190 195	
gtc ata gct ctg cga tgt gcg gtc aag gag tca aag ttc tgg agt gac	800
Val Ile Ala Leu Arg Cys Ala Val Lys Glu Ser Lys Phe Trp Ser Asp	
200 205 210	
tgg agc caa gaa aaa atg gga atg act gag gaa gaa ggc aag cta ctc	848
Trp Ser Gln Glu Lys Met Gly Met Thr Glu Glu Glu Gly Lys Leu Leu	
215 220 225	

cct gcg att ccc gtc ctg tct gct ctg gtg tagggctgct ttgggctaga 898
 Pro Ala Ile Pro Val Leu Ser Ala Leu Val
 230 235

cttgggtgggg tttgtcacca cctgggttggg aatcatggaa tctcatgacc ccagggggccc 958
 cctgtaccat cgagagtggag cctgcacaac tttgtgcccc aaaggcaaag gatcacattt 1018
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 <212> PRT
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 20 25 30
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 35 40 45
 Ser Tyr Thr Gln Tyr Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys
 50 55 60
 His Asp Asn Cys Thr Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala Ser
 65 70 75 80
 Cys Ser Phe Phe Leu Pro Arg Ile Thr Ile Pro Asp Asn Tyr Thr Ile
 85 90 95
 Glu Val Glu Ala Glu Asn Gly Asp Gly Val Ile Lys Ser His Met Thr
 100 105 110
 Tyr Trp Arg Leu Glu Asn Ile Ala Lys Thr Glu Pro Pro Lys Ile Phe
 115 120 125
 Arg Val Lys Pro Val Leu Gly Ile Lys Arg Met Ile Gln Ile Glu Trp
 130 135 140
 Ile Lys Pro Glu Leu Ala Pro Val Ser Ser Asp Leu Lys Tyr Thr Leu
 145 150 155 160
 Arg Phe Arg Thr Val Asn Ser Thr Ser Trp Met Glu Val Asn Phe Ala
 165 170 175
 Lys Asn Arg Lys Asp Lys Asn Gln Thr Tyr Asn Leu Thr Gly Leu Gln
 180 185 190
 Pro Phe Thr Glu Tyr Val Ile Ala Leu Arg Cys Ala Val Lys Glu Ser
 195 200 205
 Lys Phe Trp Ser Asp Trp Ser Gln Glu Lys Met Gly Met Thr Glu Glu
 210 215 220
 Glu Gly Lys Leu Leu Pro Ala Ile Pro Val Leu Ser Ala Leu Val
 225 230 235

<210> 23
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<220>
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<210> 24
 <211> 23
 <212> DNA
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 <220>
 <223> Oligonucleotide primer ZC27899

 <400> 24
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 <210> 25
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 <400> 25
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 <210> 26
 <211> 21
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 <220>
 <223> Oligonucleotide primer ZC17574

 <400> 26
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 <210> 27
 <211> 24
 <212> DNA
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 <220>
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 <400> 27
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 <210> 28
 <211> 25
 <212> DNA
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 <220>
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 <400> 28
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 <210> 29
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 <220>

<223> Oligonucleotide primer ZC26359
 <400> 29
 gagcagccat acaccagagc agaca 25
 <210> 30
 <211> 33
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Oligonucleotide primer ZC17212
 <400> 30
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 <210> 31
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 <220>
 <223> Oligonucleotide primer ZC17313
 <400> 31
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 <210> 32
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 <212> PRT
 <213> Artificial Sequence
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 <223> Glu-Glu Tag peptide
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 1 5
 <210> 35

<211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> FLAG tag peptide sequence

<400> 35
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 1 5

<210> 36
 <211> 699
 <212> DNA
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 acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 180
 aactggtacg tggacggcgt ggaggtgcat aatgccaaaga caaagccgcg ggaggagcag 240
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 ggcaaggagt acaagtgcga ggtctccaac aaagccctcc catcctccat cgagaaaacc 360
 atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg 420
 gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc 480
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 cccgtgctgg actccgacgg ctctctcttc ctctacagca agctcaccgt ggacaagagc 600
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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(990)

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 agc acc tct ggg ggc aca gcg gcc ctg ggc tgc ctg gtc aag gac tac 96
 Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr
 20 25 30
 ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca ggc gcc ctg acc agc 144
 Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser
 35 40 45
 ggc gtg cac acc ttc ccg gct gtc cta cag tcc tca gga ctc tac tcc 192
 Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
 50 55 60
 ctc agc agc gtg gtg acc gtg ccc tcc agc agc ttg ggc acc cag acc 240
 Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
 65 70 75 80
 tac atc tgc aac gtg aat cac aag ccc agc aac acc aag gtg gac aag 288
 Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys

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Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro				
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ctg	acc	aag	aac	cag	gtc	agc	ctg	acc	tgc	ctg	gtc	aaa	ggc	ttc	tat	768			
Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr				
245				250				255											
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260				265				270											
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Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe				
275				280				285											
ctc	tac	agc	aag	ctc	acc	gtg	gac	aag	agc	agg	tgg	cag	cag	ggg	aac	912			
Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn				
290				295				300											
gtc	ttc	tca	tgc	tcc	gtg	atg	cat	gag	gct	ctg	cac	aac	cac	tac	acg	960			
Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr				
305				310				315				320							
cag	aag	agc	ctc	tcc	ctg	tct	ccg	ggt	aaa							990			
Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys										
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 <211> 330
 <212> PRT
 <213> Homo sapiens

<400> 38
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 35 40 45
 Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser
 50 55 60
 Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr
 65 70 75 80
 Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys
 85 90 95
 Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
 100 105 110
 Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
 115 120 125
 Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
 130 135 140
 Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
 145 150 155 160
 Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
 165 170 175
 Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
 180 185 190
 His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
 195 200 205
 Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
 210 215 220
 Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
 225 230 235 240
 Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
 245 250 255
 Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
 260 265 270
 Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
 275 280 285
 Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
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 305 310 315 320
 Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 325 330

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 <212> DNA
 <213> Homo sapiens

<220>
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Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	
			20					25					30			

ccc aga gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg 144
Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser
35 40 45

ggt aac tcc cag gag agt gtc aca gag cag gac agc aag gac agc acc 192
Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr
50 55 60

tac agc ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag aaa 240
Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
65 70 75 80

cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc 288
 His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro
 85 90 95

gtc aca aag agc ttc aac agg gga gag tgt tag 321
Val Thr Lys Ser Phe Asn Arg Gly Glu Cys *
100 105

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<210> 40
<211> 106
<212> PRT
<213> Homo sapiens
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Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp 40	Lys	Val	Asp	Asn	Ala 45	Leu	Gln	Ser
Gly	Asn 50	Ser	Gln	Glu	Ser	Val 55	Thr	Glu	Gln	Asp	Ser 60	Lys	Asp	Ser	Thr
Tyr 65	Ser	Leu	Ser	Ser	Thr 70	Leu	Thr	Leu	Ser	Lys 75	Ala	Asp	Tyr	Glu	Lys 80
His	Lys	Val	Tyr	Ala 85	Cys	Glu	Val	Thr	His 90	Gln	Gly	Leu	Ser	Ser 95	Pro
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<212> DNA
<213> Artificial Sequence
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<223> Oligonucleotide primer ZC11440

<400> 41
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<211> 8
<212> DNA
<213> Artificial Sequence
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<220>
<223> Oligonucleotide primer ZC11441

<400> 42
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<210> 43
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<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC12749

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aactgtagat ttctaggaat tcaatccttg gccacgcgtc 100

<210> 44
<211> 100
<212> DNA
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<220>
<223> Oligonucleotide primer ZC12748

<400> 44
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cgcggtgtga attccgggaa ggggagggat ttacgggaag 100

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<220>
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<222> (162)...(2108)

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aaaacattct ctctccccag ccttcattgtg ttaacctggg g atg atg tgg acc tgg 176
Met Met Trp Thr Trp
1 5

gca ctg tgg atg ctc ccc tca ctc tgc aaa ttc agc ctg gca gct ctg 224
Ala Leu Trp Met Leu Pro Ser Leu Cys Lys Phe Ser Leu Ala Ala Leu
10 15 20

cca gct aag cct gag aac att tcc tgt gtc tac tac tat agg aaa aat 272
Pro Ala Lys Pro Glu Asn Ile Ser Cys Val Tyr Tyr Tyr Arg Lys Asn
25 30 35

tta acc tgc act tgg agt cca gga aag gaa acc agt tat acc cag tac 320
Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu Thr Ser Tyr Thr Gln Tyr
40 45 50

aca gtt aag aga act tac gct ttt gga gaa aaa cat gat aat tgt aca 368
Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys His Asp Asn Cys Thr
55 60 65

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acc	aat	agt	tct	aca	agt	gaa	aat	cgt	gct	tgc	tgc	tct	ttt	ttc	ctt	416
Thr	Asn	Ser	Ser	Thr	Ser	Glu	Asn	Arg	Ala	Ser	Cys	Ser	Phe	Phe	Leu	
70					75					80					85	
cca	aga	ata	acg	atc	cca	gat	aat	tat	acc	att	gag	gtg	gaa	gct	gaa	464
Pro	Arg	Ile	Thr	Ile	Pro	Asp	Asn	Tyr	Thr	Ile	Glu	Val	Glu	Ala	Glu	
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aat	gga	gat	ggt	gta	att	aaa	tct	cat	atg	aca	tac	tgg	aga	tta	gag	512
Asn	Gly	Asp	Gly	Val	Ile	Lys	Ser	His	Met	Thr	Tyr	Trp	Arg	Leu	Glu	
			105					110					115			
aac	ata	gcg	aaa	act	gaa	cca	cct	aag	att	ttc	cgt	gtg	aaa	cca	gtt	560
Asn	Ile	Ala	Lys	Thr	Glu	Pro	Pro	Lys	Ile	Phe	Arg	Val	Lys	Pro	Val	
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Leu	Gly	Ile	Lys	Arg	Met	Ile	Gln	Ile	Glu	Trp	Ile	Lys	Pro	Glu	Leu	
	135					140					145					
gcg	cct	gtt	tca	tct	gat	tta	aaa	tac	aca	ctt	cga	ttc	agg	aca	gtc	656
Ala	Pro	Val	Ser	Ser	Asp	Leu	Lys	Tyr	Thr	Leu	Arg	Phe	Arg	Thr	Val	
150					155					160					165	
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Asn	Ser	Thr	Ser	Trp	Met	Glu	Val	Asn	Phe	Ala	Lys	Asn	Arg	Lys	Asp	
				170					175					180		
aaa	aac	caa	acg	tac	aac	ctc	acg	ggg	ctg	cag	cct	ttt	aca	gaa	tat	752
Lys	Asn	Gln	Thr	Tyr	Asn	Leu	Thr	Gly	Leu	Gln	Pro	Phe	Thr	Glu	Tyr	
			185					190					195			
gtc	ata	gct	ctg	cga	tgt	gcg	gtc	aag	gag	tca	aag	ttc	tgg	agt	gac	800
Val	Ile	Ala	Leu	Arg	Cys	Ala	Val	Lys	Glu	Ser	Lys	Phe	Trp	Ser	Asp	
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tgg	agc	caa	gaa	aaa	atg	gga	atg	act	gag	gaa	gaa	gct	cca	tgt	ggc	848
Trp	Ser	Gln	Glu	Lys	Met	Gly	Met	Thr	Glu	Glu	Glu	Ala	Pro	Cys	Gly	
	215					220					225					
ctg	gaa	ctg	tgg	aga	gtc	ctg	aaa	cca	gct	gag	gcg	gat	gga	aga	agg	896
Leu	Glu	Leu	Trp	Arg	Val	Leu	Lys	Pro	Ala	Glu	Ala	Asp	Gly	Arg	Arg	
230					235					240					245	
cca	gtg	cgg	ttg	tta	tgg	aag	aag	gca	aga	gga	gcc	cca	gtc	cta	gag	944
Pro	Val	Arg	Leu	Leu	Trp	Lys	Lys	Ala	Arg	Gly	Ala	Pro	Val	Leu	Glu	
				250					255					260		
aaa	aca	ctt	ggc	tac	aac	ata	tgg	tac	tat	cca	gaa	agc	aac	act	aac	992
Lys	Thr	Leu	Gly	Tyr	Asn	Ile	Trp	Tyr	Tyr	Pro	Glu	Ser	Asn	Thr	Asn	
			265					270					275			
ctc	aca	gaa	aca	atg	aac	act	act	aac	cag	cag	ctt	gaa	ctg	cat	ctg	1040
Leu	Thr	Glu	Thr	Met	Asn	Thr	Thr	Asn	Gln	Gln	Leu	Glu	Leu	His	Leu	
		280					285					290				
gga	ggc	gag	agc	ttt	tgg	gtg	tct	atg	att	tct	tat	aat	tct	ctt	ggg	1088
Gly	Gly	Glu	Ser	Phe	Trp	Val	Ser	Met	Ile	Ser	Tyr	Asn	Ser	Leu	Gly	
	295					300					305					

aag tct cca gtg gcc acc ctg agg att cca gct att caa gaa aaa tca	1136
Lys Ser Pro Val Ala Thr Leu Arg Ile Pro Ala Ile Gln Glu Lys Ser	
310 315 320 325	
ttt cag tgc att gag gtc atg cag gcc tgc gtt gct gag gac cag cta	1184
Phe Gln Cys Ile Glu Val Met Gln Ala Cys Val Ala Glu Asp Gln Leu	
330 335 340	
gtg gtg aag tgg caa agc tct gct cta gac gtg aac act tgg atg att	1232
Val Val Lys Trp Gln Ser Ser Ala Leu Asp Val Asn Thr Trp Met Ile	
345 350 355	
gaa tgg ttt ccg gat gtg gac tca gag ccc acc acc ctt tcc tgg gaa	1280
Glu Trp Phe Pro Asp Val Asp Ser Glu Pro Thr Thr Leu Ser Trp Glu	
360 365 370	
tct gtg tct cag gcc acg aac tgg acg atc cag caa gat aaa tta aaa	1328
Ser Val Ser Gln Ala Thr Asn Trp Thr Ile Gln Gln Asp Lys Leu Lys	
375 380 385	
cct ttc tgg tgc tat aac atc tct gtg tat cca atg ttg cat gac aaa	1376
Pro Phe Trp Cys Tyr Asn Ile Ser Val Tyr Pro Met Leu His Asp Lys	
390 395 400 405	
gtt ggc gag cca tat tcc atc cag gct tat gcc aaa gaa ggc gtt cca	1424
Val Gly Glu Pro Tyr Ser Ile Gln Ala Tyr Ala Lys Glu Gly Val Pro	
410 415 420	
tca gaa ggt cct gag acc aag gtg gag aac att ggc gtg aag acg gtc	1472
Ser Glu Gly Pro Glu Thr Lys Val Glu Asn Ile Gly Val Lys Thr Val	
425 430 435	
acg atc aca tgg aaa gag att ccc aag agt gag aga aag ggt atc atc	1520
Thr Ile Thr Trp Lys Glu Ile Pro Lys Ser Glu Arg Lys Gly Ile Ile	
440 445 450	
tgc aac tac acc atc ttt tac caa gct gaa ggt gga aaa gga ttc tcc	1568
Cys Asn Tyr Thr Ile Phe Tyr Gln Ala Glu Gly Gly Lys Gly Phe Ser	
455 460 465	
aag aca gtc aat tcc agc atc ttg cag tac ggc ctg gag tcc ctg aaa	1616
Lys Thr Val Asn Ser Ser Ile Leu Gln Tyr Gly Leu Glu Ser Leu Lys	
470 475 480 485	
cga aag acc tct tac att gtt cag gtc atg gcc agc acc agt gct ggg	1664
Arg Lys Thr Ser Tyr Ile Val Gln Val Met Ala Ser Thr Ser Ala Gly	
490 495 500	
gga acc aac ggg acc agc ata aat ttc aag aca ttg tca ttc agt gtc	1712
Gly Thr Asn Gly Thr Ser Ile Asn Phe Lys Thr Leu Ser Phe Ser Val	
505 510 515	
ttt gag att atc ctc ata act tct ctg att ggt gga ggc ctt ctt att	1760
Phe Glu Ile Ile Leu Ile Thr Ser Leu Ile Gly Gly Gly Leu Leu Ile	
520 525 530	
ctc att atc ctg aca gtg gca tat ggt ctc aaa aaa ccc aac aaa ttg	1808
Leu Ile Ile Leu Thr Val Ala Tyr Gly Leu Lys Lys Pro Asn Lys Leu	
535 540 545	
act cat ctg tgt tgg ccc acc gtt ccc aac cct gct gaa agt agt ata	1856
Thr His Leu Cys Trp Pro Thr Val Pro Asn Pro Ala Glu Ser Ser Ile	

550	555	560	565	
gcc aca tgg cat gga gat gat ttc aag gat aag cta aac ctg aag gag				1904
Ala Thr Trp His Gly Asp Asp Phe Lys Asp Lys Leu Asn Leu Lys Glu	570	575	580	
tct gat gac tct gtg aac aca gaa gac agg atc tta aaa cca tgt tcc				1952
Ser Asp Asp Ser Val Asn Thr Glu Asp Arg Ile Leu Lys Pro Cys Ser	585	590	595	
acc ccc agt gac aag ttg gtg att gac aag ttg gtg gtg aac ttt ggg				2000
Thr Pro Ser Asp Lys Leu Val Ile Asp Lys Leu Val Val Asn Phe Gly	600	605	610	
aat gtt ctg caa gaa att ttc aca gat gaa gcc aga acg ggt cag gaa				2048
Asn Val Leu Gln Glu Ile Phe Thr Asp Glu Ala Arg Thr Gly Gln Glu	615	620	625	
aac aat tta gga ggg gaa aag aat ggg act aga att ctg tct tcc tgc				2096
Asn Asn Leu Gly Gly Glu Lys Asn Gly Thr Arg Ile Leu Ser Ser Cys	630	635	640	645
cca act tca ata taagtgtgga ctaaaatgcg agaaagggtgt cctgtggtct				2148
Pro Thr Ser Ile				

atgcaaatta gaaaggacat gcagagtttt ccaactagga agactgaatc tgtggcccca	2208
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gcaatctgta atgcatgtgc atgagaagtc tggtattaag tagagtgtga aaacatgggt	2328
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ataataccat tttcatgtaa tgctatactt ctatactatt ttcattgtaat actatacttc	2448
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 <212> PRT
 <213> Homo sapiens

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50 His Asp Asn Cys Thr Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala Ser	65
65 Cys Ser Phe Phe Leu Pro Arg Ile Thr Ile Pro Asp Asn Tyr Thr Ile	80
80 Glu Val Glu Ala Glu Asn Gly Asp Gly Val Ile Lys Ser His Met Thr	100
100 Tyr Trp Arg Leu Glu Asn Ile Ala Lys Thr Glu Pro Pro Lys Ile Phe	115
115 Arg Val Lys Pro Val Leu Gly Ile Lys Arg Met Ile Gln Ile Glu Trp	130
130 Ile Lys Pro Glu Leu Ala Pro Val Ser Ser Asp Leu Lys Tyr Thr Leu	145
145 Arg Phe Arg Thr Val Asn Ser Thr Ser Trp Met Glu Val Asn Phe Ala	160
165	175

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Glu	Ala	Pro	Cys	Gly	Leu	Glu	Leu	Trp	Arg	Val	Leu	Lys	Pro	Ala	Glu
225					230					235					240
Ala	Asp	Gly	Arg	Arg	Pro	Val	Arg	Leu	Leu	Trp	Lys	Lys	Ala	Arg	Gly
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Ala	Pro	Val	Leu	Glu	Lys	Thr	Leu	Gly	Tyr	Asn	Ile	Trp	Tyr	Tyr	Pro
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Glu	Ser	Asn	Thr	Asn	Leu	Thr	Glu	Thr	Met	Asn	Thr	Thr	Asn	Gln	Gln
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Leu	Glu	Leu	His	Leu	Gly	Gly	Glu	Ser	Phe	Trp	Val	Ser	Met	Ile	Ser
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Ile	Gln	Glu	Lys	Ser	Phe	Gln	Cys	Ile	Glu	Val	Met	Gln	Ala	Cys	Val
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Ala	Glu	Asp	Gln	Leu	Val	Val	Lys	Trp	Gln	Ser	Ser	Ala	Leu	Asp	Val
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Asn	Thr	Trp	Met	Ile	Glu	Trp	Phe	Pro	Asp	Val	Asp	Ser	Glu	Pro	Thr
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Met	Leu	His	Asp	Lys	Val	Gly	Glu	Pro	Tyr	Ser	Ile	Gln	Ala	Tyr	Ala
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		435					440					445			
Arg	Lys	Gly	Ile	Ile	Cys	Asn	Tyr	Thr	Ile	Phe	Tyr	Gln	Ala	Glu	Gly
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Gly	Lys	Gly	Phe	Ser	Lys	Thr	Val	Asn	Ser	Ser	Ile	Leu	Gln	Tyr	Gly
465					470					475					480
Leu	Glu	Ser	Leu	Lys	Arg	Lys	Thr	Ser	Tyr	Ile	Val	Gln	Val	Met	Ala
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Leu	Ser	Phe	Ser	Val	Phe	Glu	Ile	Ile	Leu	Ile	Thr	Ser	Leu	Ile	Gly
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Gly	Gly	Leu	Leu	Ile	Leu	Ile	Ile	Leu	Thr	Val	Ala	Tyr	Gly	Leu	Lys
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Lys	Pro	Asn	Lys	Leu	Thr	His	Leu	Cys	Trp	Pro	Thr	Val	Pro	Asn	Pro
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Ala	Glu	Ser	Ser	Ile	Ala	Thr	Trp	His	Gly	Asp	Asp	Phe	Lys	Asp	Lys
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Leu	Asn	Leu	Lys	Glu	Ser	Asp	Asp	Ser	Val	Asn	Thr	Glu	Asp	Arg	Ile
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Leu	Lys	Pro	Cys	Ser	Thr	Pro	Ser	Asp	Lys	Leu	Val	Ile	Asp	Lys	Leu
		595					600					605			
Val	Val	Asn	Phe	Gly	Asn	Val	Leu	Gln	Glu	Ile	Phe	Thr	Asp	Glu	Ala
	610					615					620				
Arg	Thr	Gly	Gln	Glu	Asn	Asn	Leu	Gly	Gly	Glu	Lys	Asn	Gly	Thr	Arg
625					630					635					640
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 <213> Artificial Sequence

<220>
 <223> Degenerate polynucleotide sequence of SEQ ID NO:46

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 acntggwsnc cnggnaarga racnwsntay acncartaya cngtnaarmg nacntaygcn 180
 ttyggngara arcaygayaa ytgyacnacn aaywsnwsna cnwsngaraa ymgngcnwsn 240
 tgywsnttyt tyytnccnmg nathacnath ccngayaayt ayacnathga rgtngargcn 300
 garaayggng ayggngtnat haarwsncay atgacntayt ggmngnytna raayathgcn 360
 aaracngarc cnccnaarat httymngtn aarccngtny tnggnathaa rmgnatgath 420
 carathgart ggathaarcc ngarytngcn ccngtnwsnw sngayytnaa rtayacnytn 480
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 ytnmgntgyg cngtnaarga rwsnaartty tggwsngayt ggwsncarga raaratgggn 660
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 wsnatgathw sntayaayws nytnngnaar wsncngtng cnacnytnmg nathccngcn 960
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 tggargara thccnaarws ngarmgnaar ggnathatht gyaaytayac nathhtytay 1380
 cargcngarg gnggnaargg nttywsnaar acngtnaayw snwsnathyt ncartayggn 1440
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 gayaarytng tnathgayaa rytngtngtn aaytyggna aygtnytnca rgarathtty 1860
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 <213> Homo sapiens

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gaatgtccgc aaaacattag ttctactctt gtcgccaggt tggagtacaa tggcacgac      180
ttggctcact gcaacctctg cctcccgggt tcaagcgatt ctctgcctc agcctcccga      240
gtagctggga ttacagttaa caataatgca atccatttcc cagcataagt gggtaagtgc      300
cactttgact tgggctgggc ttaaaagcac aagaaaagct cgcagacaat cagagtggaa      360
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gtgctgtggg aggtggagtt gcctttgatg caaatccttt gagccagcag aacatctgtg      480
gaacatcccc tgatac atg aag ctc tct ccc cag cct tca tgt gtt aac ctg      532
                Met Lys Leu Ser Pro Gln Pro Ser Cys Val Asn Leu
                  1              5              10

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Gly Met Met Trp Thr Trp Ala Leu Trp Met Leu Pro Ser Leu Cys Lys
    15              20              25

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Pro	Glu	Ser	Asn	Thr	Asn	Leu	Thr	Glu	Thr	Met	Asn	Thr	Thr	Asn	Gln	
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Gln	Leu	Glu	Leu	His	Leu	Gly	Gly	Glu	Ser	Phe	Trp	Val	Ser	Met	Ile	
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Val	Asn	Thr	Trp	Met	Ile	Glu	Trp	Phe	Pro	Asp	Val	Asp	Ser	Glu	Pro	
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Gln	Gln	Asp	Lys	Leu	Lys	Pro	Phe	Trp	Cys	Tyr	Asn	Ile	Ser	Val	Tyr	
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Pro	Met	Leu	His	Asp	Lys	Val	Gly	Glu	Pro	Tyr	Ser	Ile	Gln	Ala	Tyr	
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Gly	Gly	Lys	Gly	Phe	Ser	Lys	Thr	Val	Asn	Ser	Ser	Ile	Leu	Gln	Tyr	
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Gly	Leu	Glu	Ser	Leu	Lys	Arg	Lys	Thr	Ser	Tyr	Ile	Val	Gln	Val	Met	
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gcc	agc	acc	agt	gct	ggg	gga	acc	aac	ggg	acc	agc	ata	aat	ttc	aag	2068
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 Gly Gly Gly Leu Leu Ile Leu Ile Ile Leu Thr Val Ala Tyr Gly Leu
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 560 565 570
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 Pro Ala Glu Ser Ser Ile Ala Thr Trp His Gly Asp Asp Phe Lys Asp
 575 580 585
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 Lys Leu Asn Leu Lys Glu Ser Asp Asp Ser Val Asn Thr Glu Asp Arg
 590 595 600
 atc tta aaa cca tgt tcc acc ccc agt gac aag ttg gtg att gac aag 2356
 Ile Leu Lys Pro Cys Ser Thr Pro Ser Asp Lys Leu Val Ile Asp Lys
 605 610 615 620
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 625 630 635
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 640 645 650
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 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Lys Asn Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu Thr Ser Tyr Thr
 50 55 60
 Gln Tyr Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys His Asp Asn
 65 70 75 80
 Cys Thr Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala Ser Cys Ser Phe

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Ser	Asp	Trp	Ser	Gln	Glu	Lys	Met	Gly	Met	Thr	Glu	Glu	Glu	Ala	Pro						
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Trp	Glu	Ser	Val	Ser	Gln	Ala	Thr	Asn	Trp	Thr	Ile	Gln	Gln	Asp	Lys						
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Val	Pro	Ser	Glu	Gly	Pro	Glu	Thr	Lys	Val	Glu	Asn	Ile	Gly	Val	Lys						
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Thr	Val	Thr	Ile	Thr	Trp	Lys	Glu	Ile	Pro	Lys	Ser	Glu	Arg	Lys	Gly						
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Ile	Ile	Cys	Asn	Tyr	Thr	Ile	Phe	Tyr	Gln	Ala	Glu	Gly	Gly	Lys	Gly						
465				470			475						480								
Phe	Ser	Lys	Thr	Val	Asn	Ser	Ser	Ile	Leu	Gln	Tyr	Gly	Leu	Glu	Ser						
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[illegible]

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<211> 1986
<212> DNA
<213> Artificial Sequence
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<220>
<223> Degenerate polynucleotide sequence of SEQ ID NO:54

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<221> misc_feature
<222> (1)...(1986)
<223> n = A,T,C or G
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<400> 55

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<211> 2748

<212> DNA

<213> mus musculus

<220>

<221> CDS

<222> (237)...(2222)

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ctg agc agc cag aag gga tcc tgc agc cag gaa cca ggg gca gcc cac	287
Leu Ser Ser Gln Lys Gly Ser Cys Ser Gln Glu Pro Gly Ala Ala His	
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Val Gln Pro Leu Gly Val Asn Ala Gly Ile Met Trp Thr Leu Ala Leu	
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Trp Ala Phe Ser Phe Leu Cys Lys Phe Ser Leu Ala Val Leu Pro Thr	
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Lys Pro Glu Asn Ile Ser Cys Val Phe Tyr Phe Asp Arg Asn Leu Thr	
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tgc act tgg aga cca gag aag gaa acc aat gat acc agc tac att gtg	479
Cys Thr Trp Arg Pro Glu Lys Glu Thr Asn Asp Thr Ser Tyr Ile Val	
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Thr Leu Thr Tyr Ser Tyr Gly Lys Ser Asn Tyr Ser Asp Asn Ala Thr	
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Glu Ala Ser Tyr Ser Phe Pro Arg Ser Cys Ala Met Pro Pro Asp Ile	
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Cys Ser Val Glu Val Gln Ala Gln Asn Gly Asp Gly Lys Val Lys Ser	
115 120 125	
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Ile Ile Leu Ser Val Asn Pro Ile Cys Asn Arg Met Phe Gln Ile Gln	
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Trp Lys Pro Arg Glu Lys Thr Arg Gly Phe Pro Leu Val Cys Met Leu	
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Arg Phe Arg Thr Val Asn Ser Ser Arg Trp Thr Glu Val Asn Phe Glu	
180 185 190	

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Tyr	Val	Leu	Ala	Leu	Arg	Phe	Arg	Phe	Asn	Asp	Ser	Arg	Tyr	Trp	Ser	
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Val	Leu	Asp	Leu	Trp	Arg	Ile	Leu	Glu	Pro	Ala	Asp	Met	Asn	Gly	Asp	
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Arg	Lys	Val	Arg	Leu	Leu	Trp	Lys	Lys	Ala	Arg	Gly	Ala	Pro	Val	Leu	
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Gly	Lys	Ser	Gln	Glu	Thr	Ile	Leu	Arg	Ile	Pro	Asp	Val	His	Glu	Lys	
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Thr	Phe	Gln	Tyr	Ile	Lys	Ser	Met	Gln	Ala	Tyr	Ile	Ala	Glu	Pro	Leu	
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Val	Glu	Trp	Leu	Pro	Glu	Ala	Ala	Met	Ser	Lys	Phe	Pro	Ala	Leu	Ser	
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cac	cga	gtt	gga	gag	ccg	tat	tca	atc	caa	gct	tat	gcc	aaa	gaa	gga	1535
His	Arg	Val	Gly	Glu	Pro	Tyr	Ser	Ile	Gln	Ala	Tyr	Ala	Lys	Glu	Gly	
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35 40 45
Thr Lys Pro Glu Asn Ile Ser Cys Val Phe Tyr Phe Asp Arg Asn Leu
50 55 60
Thr Cys Thr Trp Arg Pro Glu Lys Glu Thr Asn Asp Thr Ser Tyr Ile
65 70 75 80
Val Thr Leu Thr Tyr Ser Tyr Gly Lys Ser Asn Tyr Ser Asp Asn Ala
85 90 95
Thr Glu Ala Ser Tyr Ser Phe Pro Arg Ser Cys Ala Met Pro Pro Asp
100 105 110
Ile Cys Ser Val Glu Val Gln Ala Gln Asn Gly Asp Gly Lys Val Lys
115 120 125
Ser Asp Ile Thr Tyr Trp His Leu Ile Ser Ile Ala Lys Thr Glu Pro
130 135 140
Pro Ile Ile Leu Ser Val Asn Pro Ile Cys Asn Arg Met Phe Gln Ile
145 150 155 160
Gln Trp Lys Pro Arg Glu Lys Thr Arg Gly Phe Pro Leu Val Cys Met
165 170 175
Leu Arg Phe Arg Thr Val Asn Ser Ser Arg Trp Thr Glu Val Asn Phe
180 185 190
Glu Asn Cys Lys Gln Val Cys Asn Leu Thr Gly Leu Gln Ala Phe Thr
195 200 205
Glu Tyr Val Leu Ala Leu Arg Phe Arg Phe Asn Asp Ser Arg Tyr Trp
210 215 220
Ser Lys Trp Ser Lys Glu Glu Thr Arg Val Thr Met Glu Glu Val Pro
225 230 235 240
His Val Leu Asp Leu Trp Arg Ile Leu Glu Pro Ala Asp Met Asn Gly
245 250 255
Asp Arg Lys Val Arg Leu Leu Trp Lys Lys Ala Arg Gly Ala Pro Val
260 265 270
Leu Glu Lys Thr Phe Gly Tyr His Ile Gln Tyr Phe Ala Glu Asn Ser
275 280 285
Thr Asn Leu Thr Glu Ile Asn Asn Ile Thr Thr Gln Gln Tyr Glu Leu
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305 310 315 320
Leu Gly Lys Ser Gln Glu Thr Ile Leu Arg Ile Pro Asp Val His Glu
325 330 335
Lys Thr Phe Gln Tyr Ile Lys Ser Met Gln Ala Tyr Ile Ala Glu Pro
340 345 350
Leu Leu Val Val Asn Trp Gln Ser Ser Ile Pro Ala Val Asp Thr Trp
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Ile Val Glu Trp Leu Pro Glu Ala Ala Met Ser Lys Phe Pro Ala Leu
370 375 380
Ser Trp Glu Ser Val Ser Gln Val Thr Asn Trp Thr Ile Glu Gln Asp

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385          390          395          400
Lys Leu Lys Pro Phe Thr Cys Tyr Asn Ile Ser Val Tyr Pro Val Leu
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Gly His Arg Val Gly Glu Pro Tyr Ser Ile Gln Ala Tyr Ala Lys Glu
          420          425          430
Gly Thr Pro Leu Lys Gly Pro Glu Thr Arg Val Glu Asn Ile Gly Leu
          435          440          445
Arg Thr Ala Thr Ile Thr Trp Lys Glu Ile Pro Lys Ser Ala Arg Asn
          450          455          460
Gly Phe Ile Asn Asn Tyr Thr Val Phe Tyr Gln Ala Glu Gly Gly Lys
465          470          475          480
Glu Leu Ser Lys Thr Val Asn Ser His Ala Leu Gln Cys Asp Leu Glu
          485          490          495
Ser Leu Thr Arg Arg Thr Ser Tyr Thr Val Trp Val Met Ala Ser Thr
          500          505          510
Arg Ala Gly Thr Asn Gly Val Arg Ile Asn Phe Lys Thr Leu Ser
          515          520          525
Ile Ser Val Phe Glu Ile Val Leu Leu Thr Ser Leu Val Gly Gly Gly
530          535          540
Leu Leu Leu Leu Ser Ile Lys Thr Val Thr Phe Gly Leu Arg Lys Pro
545          550          555          560
Asn Arg Leu Thr Pro Leu Cys Cys Pro Asp Val Pro Asn Pro Ala Glu
          565          570          575
Ser Ser Leu Ala Thr Trp Leu Gly Asp Gly Phe Lys Lys Ser Asn Met
          580          585          590
Lys Glu Thr Gly Asn Ser Gly Asn Thr Glu Asp Val Val Leu Lys Pro
          595          600          605
Cys Pro Val Pro Ala Asp Leu Ile Asp Lys Leu Val Val Asn Phe Glu
610          615          620
Asn Phe Leu Glu Val Val Leu Thr Glu Glu Ala Gly Lys Gly Gln Ala
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21

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<210> 67
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acc tgg gca ctg tgg atg ctc cct tca ctc tgc aaa ttc agc ctg gca 96
Thr Trp Ala Leu Trp Met Leu Pro Ser Leu Cys Lys Phe Ser Leu Ala
20 25 30

gct ctg cca gct aag cct gag aac att tcc tgt gtc tac tac tat agg 144
Ala Leu Pro Ala Lys Pro Glu Asn Ile Ser Cys Val Tyr Tyr Tyr Arg
35 40 45

aaa aat tta acc tgc act tgg agt cca gga aag gaa acc agt tat acc 192
Lys Asn Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu Thr Ser Tyr Thr
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cag tac aca gtt aag aga act tac gct ttt gga gaa aaa cat gat aat 240
Gln Tyr Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys His Asp Asn
65 70 75 80

tgt aca acc aat agt tct aca agt gaa aat cgt gct tcg tgc tct ttt 288
Cys Thr Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala Ser Cys Ser Phe
85 90 95

ttc ctt cca aga ata acg atc cca gat aat tat acc att gag gtg gaa 336
Phe Leu Pro Arg Ile Thr Ile Pro Asp Asn Tyr Thr Ile Glu Val Glu
100 105 110

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Leu Glu Asn Ile Ala Lys Thr Glu Pro Pro Lys Ile Phe Arg Val Lys	
130 135 140	
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Pro Val Leu Gly Ile Lys Arg Met Ile Gln Ile Glu Trp Ile Lys Pro	
145 150 155 160	
gag ttg gcg cct gtt tca tct gat tta aaa tac aca ctt cga ttc agg	528
Glu Leu Ala Pro Val Ser Ser Asp Leu Lys Tyr Thr Leu Arg Phe Arg	
165 170 175	
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Thr Val Asn Ser Thr Ser Trp Met Glu Val Asn Phe Ala Lys Asn Arg	
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Lys Asp Lys Asn Gln Thr Tyr Asn Leu Thr Gly Leu Gln Pro Phe Thr	
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Cys Gly Leu Glu Leu Trp Arg Val Leu Lys Pro Ala Glu Ala Asp Gly	
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Arg Arg Pro Val Arg Leu Leu Trp Lys Lys Ala Arg Gly Ala Pro Val	
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275 280 285	
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His Leu Gly Gly Glu Ser Phe Trp Val Ser Met Ile Ser Tyr Asn Ser	
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Leu Gly Lys Ser Pro Val Ala Thr Leu Arg Ile Pro Ala Ile Gln Glu	
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Lys Ser Phe Gln Cys Ile Glu Val Met Gln Ala Cys Val Ala Glu Asp	
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Gln Leu Val Val Lys Trp Gln Ser Ser Ala Leu Asp Val Asn Thr Trp	

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gac aaa gtt ggc gag cca tat tcc atc cag gct tat gcc aaa gaa ggc Asp Lys Val Gly Glu Pro Tyr Ser Ile Gln Ala Tyr Ala Lys Glu Gly 420 425 430			1296
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aca tgc gtg gtg gtg gac gtg agc cac gaa gac cct gag gtc aag ttc Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe 580 585 590			1776
aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag aca aag ccg Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro 595 600 605			1824

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Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
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gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc      1920
Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
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tcc aac aaa gcc ctc cca tcc tcc atc gag aaa acc atc tcc aaa gcc      1968
Ser Asn Lys Ala Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala
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aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc cca tcc cgg      2016
Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
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gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc      2064
Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
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ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg cag ccg      2112
Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
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gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac ggc tcc      2160
Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
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ttc ttc ctc tac agc aag ctc acc gtg gac aag agc agg tgg cag cag      2208
Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
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ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac      2256
Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
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Gln Tyr Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys His Asp Asn
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Cys Thr Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala Ser Cys Ser Phe
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Glu	Leu	Ala	Pro	Val	Ser	Ser	Asp	Leu	Lys	Tyr	Thr	Leu	Arg	Phe	Arg
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Cys	Gly	Leu	Glu	Leu	Trp	Arg	Val	Leu	Lys	Pro	Ala	Glu	Ala	Asp	Gly
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Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly			
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tgg gca ttc	tct ttc ctc	tgc aaa	ttc agc	ctg gca	gtc ctg	ccg act	383
Trp Ala Phe	Ser Phe Leu	Cys Lys	Phe Ser	Leu Ala	Val Leu	Pro Thr	
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aag cca gag	aac att tcc	tgc gtc	ttt tac	ttc gac	aga aat	ctg act	431
Lys Pro Glu	Asn Ile Ser	Cys Val	Phe Tyr	Phe Asp	Arg Asn	Leu Thr	
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tgc act tgg	aga cca gag	aag gaa	acc aat	gat acc	agc tac	att gtg	479
Cys Thr Trp	Arg Pro Glu	Lys Glu	Thr Asn	Asp Thr	Ser Tyr	Ile Val	
	70		75			80	

act ttg act	tac tcc tat	gga aaa	agc aat	tat agt	gac aat	gct aca	527
Thr Leu Thr	Tyr Ser Tyr	Gly Lys	Ser Asn	Tyr Ser	Asp Asn	Ala Thr	
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Glu Ala Ser	Tyr Ser Phe	Pro Arg	Ser Cys	Ala Met	Pro Pro	Asp Ile	
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gac Asp 130	atc Ile	aca Thr	tat Tyr	tgg Trp	cat His 135	tta Leu	atc Ile	tcc Ser	ata Ile	gca Ala 140	aaa Lys	acc Thr	gaa Glu	cca Pro	cct Pro 145	671
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Leu	Thr	Arg	Arg	Thr	Ser	Tyr	Thr	Val	Trp	Val	Met	Ala	Ser	Thr	Arg	
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Thr Lys Pro Glu Asn Ile Ser Cys Val Phe Tyr Phe Asp Arg Asn Leu
50 55 60
Thr Cys Thr Trp Arg Pro Glu Lys Glu Thr Asn Asp Thr Ser Tyr Ile
65 70 75 80
Val Thr Leu Thr Tyr Ser Tyr Gly Lys Ser Asn Tyr Ser Asp Asn Ala
85 90 95
Thr Glu Ala Ser Tyr Ser Phe Pro Arg Ser Cys Ala Met Pro Pro Asp
100 105 110
Ile Cys Ser Val Glu Val Gln Ala Gln Asn Gly Asp Gly Lys Val Lys
115 120 125
Ser Asp Ile Thr Tyr Trp His Leu Ile Ser Ile Ala Lys Thr Glu Pro
130 135 140
Pro Ile Ile Leu Ser Val Asn Pro Ile Cys Asn Arg Met Phe Gln Ile
145 150 155 160
Gln Trp Lys Pro Arg Glu Lys Thr Arg Gly Phe Pro Leu Val Cys Met
165 170 175
Leu Arg Phe Arg Thr Val Asn Ser Ser Arg Trp Thr Glu Val Asn Phe
180 185 190
Glu Asn Cys Lys Gln Val Cys Asn Leu Thr Gly Leu Gln Ala Phe Thr
195 200 205
Glu Tyr Val Leu Ala Leu Arg Phe Arg Phe Asn Asp Ser Arg Tyr Trp
210 215 220
Ser Lys Trp Ser Lys Glu Glu Thr Arg Val Thr Met Glu Glu Val Pro
225 230 235 240
His Val Leu Asp Leu Trp Arg Ile Leu Glu Pro Ala Asp Met Asn Gly
245 250 255
Asp Arg Lys Val Arg Leu Leu Trp Lys Lys Ala Arg Gly Ala Pro Val
260 265 270
Leu Glu Lys Thr Phe Gly Tyr His Ile Gln Tyr Phe Ala Glu Asn Ser
275 280 285
Thr Asn Leu Thr Glu Ile Asn Asn Ile Thr Thr Gln Gln Tyr Glu Leu
290 295 300
Leu Leu Met Ser Gln Ala His Ser Val Ser Val Thr Ser Phe Asn Ser
305 310 315 320
Leu Gly Lys Ser Gln Glu Thr Ile Leu Arg Ile Pro Asp Val His Glu
325 330 335
Lys Thr Phe Gln Tyr Ile Lys Ser Met Gln Ala Tyr Ile Ala Glu Pro
340 345 350
Leu Leu Val Val Asn Trp Gln Ser Ser Ile Pro Ala Val Asp Thr Trp
355 360 365
Ile Val Glu Trp Leu Pro Glu Ala Ala Met Ser Lys Phe Pro Ala Leu
370 375 380
Ser Trp Glu Ser Val Ser Gln Val Thr Asn Trp Thr Ile Glu Gln Asp
385 390 395 400
Lys Leu Lys Pro Phe Thr Cys Tyr Asn Ile Ser Val Tyr Pro Val Leu
405 410 415
Gly His Arg Val Gly Glu Pro Tyr Ser Ile Gln Ala Tyr Ala Lys Glu

Condition	Control (%)	MCI (%)	AD (%)
A	~95	~95	~95
B	~95	~85	~75
C	~95	~85	~75
D	~95	~85	~75

